



1/8

GGGGGATCATGGAAGCTGATAAAGATGACACACAACAAATTCTTAAGGAGCATTGCCAGATGAA  
TTTATAAAAGATGAACAAAATAAGGGACTAATTGATGAAATTACAAAGAAAAATATTCAACTAAA  
GAAGGAGATCCAAAAGCTTGAAACGGAGTTACAAGAGGCTACCAAAGAATTCCAGATTAAAGAGG  
ATATTCCTGAAACAAAGATGAAATTCTTATCAGTTGAAACTCCTGAGAATGACAGCCAGTTGTCA  
AATATCTCCTGTTTCGTTTCAAGTGAGCTCGAAAGTTCCTTATGAGATACAAAAGGACAAGCACT  
TATCACCTTTGAAAAAGAAGAAGTTGCTCAAATGTGGTAAGCATGAGTAAACATCATGTACAGA  
TAAAAGATGTAAATCTGGAGGTTACGGCCAAGCCAGTTCCATTAAATTCAGGAGTCAGATTCCAG  
GTTTATGTAGAAGTTTCTAAAATGAAAATCAATGTTACTGAAATTCCTGACACATTGCGTGAAGA  
TCAAATGAGAGACAACTAGAGCTGAGCTTTTCAAAGTCCCGAAATGGGAGGCGGAGANGTGGAC  
CGCGTGGGACTATGACAGACAGTCCGGGAGTGCAGTCATCACGTTTGGNGGAGATTGGGAGTGGC  
TGACANN (SEQ ID NO:4)

**Figure 1**

Hou c6/#1



2/8

CGGAGTTACAAGAGGCTACCAAAGAATTCCAGATTAAAGAGGATATTCCTGAAACAAAGATGAAA  
TTCTTATCAGTTGAAACTCCTGANAATGACAGCCAGTTGTCAAATATCTCCTGTTTCGTTTCAAGG  
TGAGCTCGAAAGTTCCTTATGAGATACAAAAAGGACAATGCACTTATCACCTTTGAAAAAGGAAG  
AAGTTGCTCAAAATGTGNGTAANGCATGAGTAAACATCATGTACAGATAATAAGATGTAAATCTG  
GAGGTTACGGCCAAAGCCAAGTTCCTTAATATTCAAGGAGTCANGATTCCAGNGTTTATGCTAG  
AANGTTTCTAAAAATGANAATCAATGGTTACTGGAAATTCTTGGACACATTGCGNTGAAAGATCA  
AGATGACGAAGACAACTAAGAAGCTGAGCTTTTCAAAGTCCCGAAANATGGAAGAGCGGTAGA  
GGGTGGNACCGCGTGNGANCTATGACAAGACAAGNCCGGGGAAGNTGCAGTCCATCACGTTTGTN  
NGAAGATTGGANGTNGGCTGACCAANGAATTTTGAAAAAGGAGANGAATTACCCCTCTTTANGAG  
TAANATCAAAACCCTGCCATAANAAGTTNACTGGTTTCNCCCATTACACAGNAN  
TTACANNNTGANCAANANTANNCAGGATAATTTNCAGGGGAANAATCTNAAGNATGGCAAGNTGA  
CTTCTGGACAANGGT (SEQ ID NO:5)

**Figure 2**

Hou c17/#2



c6/#1	1	HEGRCI	MEADKDDTQQILKEHSPDEFIKDEQNKGLIDEITKKNIQLKKEIQKLETELQEA
Hou/Nmi	1	-----	MEADKDDTQQILKEHSPDEFIKDEQNKGLIDEITKKNIQLKKEIQKLETELQEA
c6/#1	61	TKEFQIKEDIPETKMKFLSVETPENDSQLSNISCSFQVSSKVPYEIQKGQALITFEKEEV	
Hou/Nmi	55	TKEFQIKEDIPETKMKFLSVETPENDSQLSNISCSFQVSSKVPYEIQKGQALITFEKEEV	
c6/#1	121	AQNVVSMKHHVQIKDVNLEVTAKEPVPLNSGVRFQVYVEVSKMKINVTEIPDTLREDQMR	
Hou/Nmi	115	AQNVVSMKHHVQIKDVNLEVTAKEPVPLNSGVRFQVYVEVSKMKINVTEIPDTLREDQMR	
c6/#1	181	DKLELSFSKSRNGRRRCGPRTMTDSPGVQSSRLVEIGS	-----
Hou/Nmi	175	DKLELSFSKFRNGGGEV.DVVDYDRQS	SAVITFVEIGV DKILAKKEYPLYINQTCHRV
c6/#1	221	-----	-----
Hou/Nmi	234	TVSPYTEIHLKKYQIFSGTSKRTVLLTGMEGIQMDREIVEDLINIHFORAKNGGGEVDVV	
c6/#1	221	-----	(SEQ ID NO:6)
Hou/Nmi	294	KCSLGQPHIAYFEE	(SEQ ID NO:7)

Figure 3



4/8

AGCAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGCAGGTC  
CAGCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGTCCAGCCAGTTGAGTGGCCGGAGGGT  
GTTGGTCACTGGATTTCCCTGCCAGCCTCAGGCTGAGTGAGGAGGAGCTGCTGGACAANCTANAGA  
TCTTCTTTGGCAAGACTAGGAACGGAGGTGGCNATGTGGACNTTCGGGANCTACTGCCAGGGANT  
GTCATGCTGGGGTTTGTAGGGATGGAGTGGCTCANCCTGTGTGCCAAATCGGCCATTTACAGT  
GCCACTGGGTGGGCAGCANGTCCCTCTGAGAGTCTCTCCGTATGTGAATGGGGANATCCAGANGG  
CTGANATCAGGTCNCAGCCANTTCCCCGCTCGGTACTGGTGCTCAACATTCCTGATATCTTGGAT  
GGCCCGGAGCTGCATGACGTCCTGGANATCCACTTCCAGAANCCACCCGCGGGGGCGGAGATGT  
AAGACGCCCTGACAGTCGTACCCCAAGGACAACAGGGCCTAACAGTCTTCACCTCCTGAATCAAG  
GCTANGGGCCTCCCCCTTCTCATCCTCCCCACCCCCCGCCAAAGGTTCTCAANACTGGGCCTG  
GGCTTTNTG (SEQ ID NO:8)

Figure 4

IFP35 c14/#1



5/8

CCAAAGTGGCTGAGCAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGC  
AGGTCCAGCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGTCCAGCCAGTTGAGTGGCCGGAGGGTGT  
TGGTCACTGGATTTCTGCCAGCCTCAGGCTGAGTGAGGAGGAGCTGCTGGACAAGCTAGAGATCTTCTTTG  
GCAAGACTAGGAACGGAGGTGGCGATGTGGACGTTCTGGGAGCTACTGCCAGGGAGTGTGCTGCTGGGGTTTG  
CTAGGGATGGAGTGGCTCAGCGTCTGTGCCAAATCGGCCAAGTTCACAGTGCCACTGGGTGGGCANCAAGTC  
CCTCTGAGAGTCTCTCCGTATGTGAATGGGGAGATCCAGAAGGCTGAGATCAGGTTCGCANCCAGTTCCCCNC  
TCGGTACTGGGTGCTCAACATTCCTGATATCTTGGATTGGCCCGGAGCTGCATNACGTCCTGGANATCAACT  
TCANAAGCCCACCCGCCGGGCGNGAGGTANAAGGCCTGACATCNTTACCCCAAAGGACAGCATGGNCCTA  
ACAGTCCTCACCTCCNAATCANGCTNNGGGGCTNCCCTTCTANCNTCCCCAACTG (SEQ ID NO:9)

**Figure 5**

IFP35 c33/#2



6/8

GGATCCACTGCCCTCTGCTTGCGGGCTCTGCTCTGATCACCTTTGATGACCCCAAAGTGGCTGAG  
CAGGTGCTGCAACAAAAGGAGCACACGATCAACATGGAGGAGTGCCGGCTGCGGGTGCAGGTCCA  
GCCCTTGGAGCTGCCCATGGTCACCACCATCCAGGTGATGGTGTCCAGCCANTTGAGTGGCCGGA  
GGGTGTTGGTCACTGGATTTCCTGCCAGCCTCAGGCTGANTGAGGAGGAGCTGCTGGACAAGCTA  
TGAGATCTTCTTTGGCAANACTANGAACGGANGTGGCGATGTGGACGTTTCGGGAGCTACTGCCAG  
GGAGTGTGATGCTGGGGTTTGCTACGGATGGAGTGGCTCAGCGTCTGTGCCAAATCGGCCAGTTC  
ACAAGTGCCACTGGGTGGGCAGCAAGTCCCTCTGAGAGTCTCTCCGTATGTGANTGGNGAGATCA  
GAATGCTGANATTAAGTCGCATCCAATTCTCGCTCNGGTACTGGTGCTCANNATCCTGANATCT  
TGGATTGGCCCCNGANTNCATGANATCTGGNAGATTCAATTNCANAAGTCCANCCNNCNGNGNCG  
GGAAGTANANGCCCGANANTTCNTNNCNTANGGNCAGCANNGCCTG (SEQ ID NO:10)

**Figure 6**

IFP35 c51/#3



```
331fn 1 -----MSAPLDAALHAQZQARLKMRLWDLQQLKXELQDSPKDKVPFSVPKIPLVFRGHTQQDP-----
In35_Human 1
CS1 1

331fn 1 -----HECPKVAEQVLQCKEHTINMEECRRLRVQVQPLELPM-----
In35_Human 61 EVPKSLVSNLRHKCPCLLAGSALITFDDPKVAEQVLQCKEHTINMEECRRLRVQVQPLELPM
CS1 1 -----HECRHKCPCLLAGSALITFDDPKVAEQVLQCKEHTINMEECRRLRVQVQPLELPM-----

331fn 37 VTTIQ..VSSQLSGRRVLVTGFPASLRLSEELLDKLEIFFGKTRNGGGDGDVRELLPGS-----
In35_Human 121 VTTIQ..VSSQLSGRRVLVTGFPASLRLSEELLDKLEIFFGKTRNGGGDGDVRELLPGS
CS1 54 VTTIQVMVSSXLSGRRVLVTGFPASLRLKEEELLDKLI*DLLWQXXKXWRC.....

331fn 95 VMLGFARDGVAQRLCQICQVHSAATCMWASSPSZSHSVCEWQDPFQ-----
In35_Human 179 VMLGFARDGVAQRLCQICQVHSAATCMWASSPSZSHSVCEWQDPFQ-----
CS1 104 .....GRSGATARECHAGVCYCWEGSGASVPRPVRHSGEYVGSKEI*ESLRM*XXRSEC*X
(SAQ ID NO:11)

331fn 139 -----PDILDPPELHDVLEIHFQKPTAGCGGCGPDSRTPTAGPSSLHL-----
In35_Human 239 PDILDPPELHDVLEIHFQKPTAGCGGCGPDSRTPTAGPSSLHL-----
CS1 156 +VASNSSLIYWCXSIS*ALGLAPXXMXSGRPNXISPIIXXOKXIPXXSXXXXXIA (SEQ ID NO:12)
(SAQ ID NO:13)
```

Figure 7



8/8

Abp2	1	RLRNQHVGISFVPKETGEHLVHVKKNGQHVASSPIPVVISQSEIGDASRVVSGQGLHEG
C50	1	-----
C57	1	-----
Abp2	61	HTFEPAEFIIIDTRDAGYGGLSLSIEGFSKVDINTEDLEDGTCRVTYCPTTEPGNYIINIKF
C50	1	-----
C57	1	-----HEGRPTTEPGNYIINIKF
Abp2	121	ADQHVPGPSFVSVKVTGEGRVKESITRRRRAPSVANVGSHCDLSLKIPEISIQDMTAQVTS
C50	1	-----
C57	18	ADQHVPGPSFVSVKVTGEGRVKESITRRRRAPSVANVGSHCDLSLKIPEISIQDMTAQVTS
Abp2	181	PSGKTHEAEIVEGENHTYCIREFVPAEMGTHTVSVKYKGQHVPGSPFFQFTVGPLGEGGAHK
C50	1	-----
C57	78	PSGKTHEAEIVEGENHTYCIREFVPAEMGTHTVSVKYKGQHVPGSPFFQFTVGPLGEGGAHX
Abp2	241	VRAGGPGLLENEGVPFEFS.WTREAGAGGLAVEDEKAEISFEDRQDSCGWAYVV
C50	1	-----
C57	138	VRAGGPGLXKE*WASARIQYTGPGKLVLEWPELSXNPELXSLLRATAPVVLMEV
Abp2	300	QEPGDYEVSVKFNEEHIPDSPPVVPVASPSGDARRLTVSSSLQESGLKVNQPASFVSLNG
C50	1	-----
C57	197	XEPSD*XNPXQVSTKEHX-----
Abp2	360	AKGAIDAKVHSPSGALEECYVTEIDQDKYAVRFIPRENGVYLIDVKFNGTHIPGSPFKIR
C50	1	-----
C57	214	-----
Abp2	420	VGEFGHGGDPGLVSAYGAGLEG.GVTGNPAEFVVNTSNAGAGALSVTIDGPSKVKMDCQE
C50	1	-----HEGRGVTCNPAEFVVNTSNAGAGALSVTIDGPSKVKMDCQE
C57	214	-----
Abp2	479	CPEGYRVTYTPMAPGSYLSISKYGGPYHIGGSPFKAKVTGPRLVSNHSLHETSSVFVDSL
C50	42	CPEGYRVTYTPMAPGSYLSISKYGGPYHIGGSPFKAKVTGPRLVSNHSLHETSSVFVDSL
C57	214	-----
Abp2	539	TKATCAPQHGAEPGPGPADASKVVAKGLGLSKAYVQOKSFTVDCSKAGNMMLLVGVHGPW
C50	102	TKATCAPHHGAEPGPGPADASKVVAKGLGLSKAYVCHKSFTVDCSKACIIMLLVGVBGPW
C57	214	-----
Abp2	599	TPCEILVKRVGS.RLYSVSYLLKDKGE.YTLVVKWCHHEHFGSPYRVVVP- (SEQ ID NO:14)
C50	162	TPCEILVKARGQFATQRVLTCTFKDKGEVHTGGQNGCDYQIPCKPLPTCGCP (SEQ ID NO:15)
C57	214	----- (SEQ ID NO:16)

Figure 8